

$1/24$

$2/24$	$3/24$
$4/24$	$5/24$
$6/24$	$7/24$

Fig. 1

2/24

-60 tgaaaagatagaataaatggcctcgtg
1 ATGGCGCGGCCAGCGCTGCTGGGCGAG
1 M A R P A L L G E
61 GGCCAAGTTGCCGCGGCCACAGAAGTT
21 C Q V A A A T E V
121 GAAAATCTCTGCACGATAATATGGACG
41 E N L C T I I W T
181 ACTCTCAGATATTTTAGTCACTTTGAT
61 T L R Y F S H F D
241 CATCGTAAAGAGGAATTACCCCTGGAT
81 H R K E E L P L D
301 AGTGCCAATGAAAGTGAGAAGCCTAGC
101 S A N E S E K P S
361 GGTGATCCTGAGTCCGCTGTGACTGAG
121 G D P E S A V T E
421 AAGTGTTCTGCTCCCTGGAAGGAAT
141 K C S W L F G R N

Fig. 1(i)

3/24

ccgaattcggcaccgagccgagggcgaggggcctgc

CTGTTGGTGCTGCTACTGTGGACCGCCACCGTG

L L V L L L W T A T V

CAGCCACCTGTGACGAATTTGAGCGTCTCTGTG

Q P P V T N L S V S V

TGGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

GACCAACAGGATAAGAAAATTGCTCCAGAAACT

D Q Q D K K I A P E T

GAGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT

E K I C L Q V G S Q C

CCTTTGGTGAAAAAGTGCATCTCACCCCCCTGAA

P L V K K C I S P P E

CTCAAGTGCATTTGGCATAACCTGAGCTATATG

L K C I W H N L S Y M

ACAAGCCCTGACACACACTATACTCTGTACTAT

T S P D T H Y T L Y Y

Fig. 1(II)

4/24

481	TGGTACAGCAGCCTGGACAAAAGTCGT
161	W Y S S L E K S R
541	ATTGCTTGTTTCCTTTAAATTGACTAAA
181	I A C S F K L T K
601	ATAATGGTCAAGGATAATGCTGGGAAA
201	I M V K D N A G K
661	TCCTATGTGAAACCTGATCCTCCACAT
221	S Y V K P D P P H
721	TTAGTGCAGTGGAAGAATCCACAAAAT
241	L V Q W K N P Q N
781	GTCAATAATACTCAAACCGACCGACAT
261	V N N T Q T D R H
841	AATTCCGAATCTGATAGAAACATGGAG
281	N S E S D R N M E
901	GCCGACGCTGTCTACACAGTCAGAGTA
301	A D A V Y T V R V
961	AACAAACTGTGGAGTGATTGGAGTGAA
321	N K L W S D W S E

Fig. 1(iii)

5/24

CAATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H
GTGGAACCTAGTTTTGAACATCAGAACGTTCAA
V E P S F E H Q N V Q
ATTAGGCCATCCTGCAAAATAGTGTCTTTAACT
I R P S C K I V S L T
ATTAAACATCTTCTCCTCAAAAATGGTGCCTTA
I K H L L L K N G A L
TTTAGAAGCAGATGCTTAACCTTATGAAGTGGAG
F R S R C L T Y E V E
AATATTTTAGAGGTTGAAGAGGACAAATGCCAG
N I L E V E E D K C Q
GGTACAAGTTGTTTCCAACCTCCCTGGTGTCTT
G T S C F Q L P G V L
AGAGTCAAAACAAACAAGTTATGCTTTGATGAC
R V K T N K L C F D D
GCACAGAGTATAGGTAAGGAGCAAAACTCCACC

Fig. 1(iv)

6/24

1021	<u>TTCTACACCACCATGTTACTCACCATT</u>
341	<u>F Y T T M L L T I</u>
1081	<u>CTTTTITACCTGAAAAGGCTTAAGATC</u>
361	<u>L F Y L K R L K I</u>
1141	ATTTTAAAGAAATGTTTGGAGACCAG
381	I F K E M F G D Q
1201	ATCTATGAGAAACAATCCAAAGAAGAA
401	I Y E K Q S K E E
1261	AAAGCAGCTCCTTGATgggggagaagtg
421	K A A P *
1321	gatttattgcattctccatttggttatc
1381	cttgaaaaacaggcagctcctaagagc
1441	ccaaacccaaaggagctccttccaaga
1501	ccctaaaagcagatgttttgccaaatc
1561	accatcaattcatctaatacaggaattg

Fig. 1(v)

7/24

CCAGTCTTTGTCGCGCAGTGGCAGTCATAATCCTC
P V F V A V A V I I L

ATTATATTTCTCCAATTCCTGATCCTGGCAAG¹
I I F P P I P D P G K

AATGATGATACCCTGCACTGGAAGAAGTATGAC
N D D T L H W K K Y D

ACGGATTCTGTAGTGCTGATAGAAAACCTGAAG
T D S V V L I E N L K

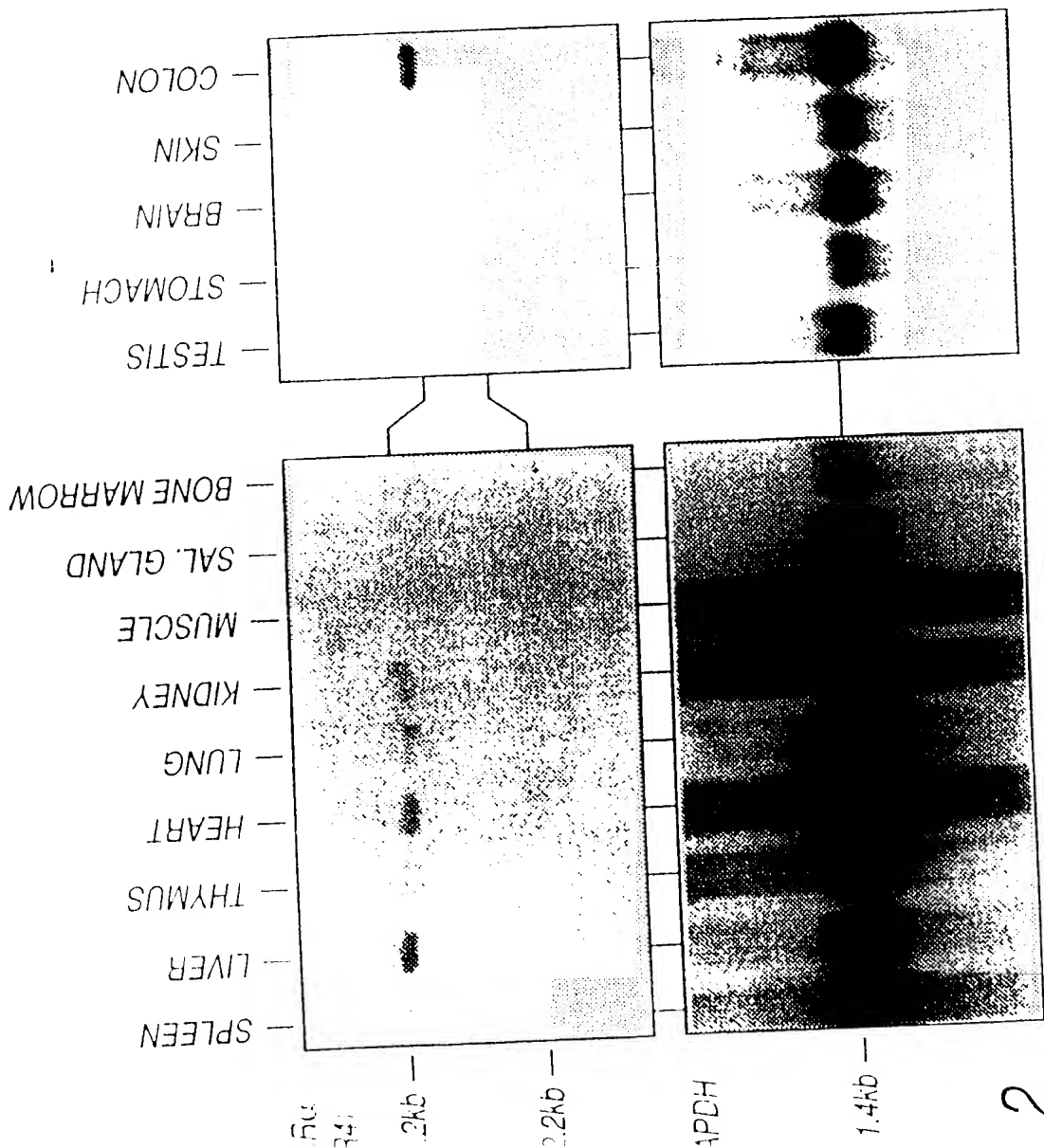
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cccaaactagaggacaaagacaaggggacaatg
tgatggcttcctaaggaatctctgcttgctctg

Fig. 1(vi)

8/24

NR4 EXPRESSION IN MOUSE TISSUES



9/24

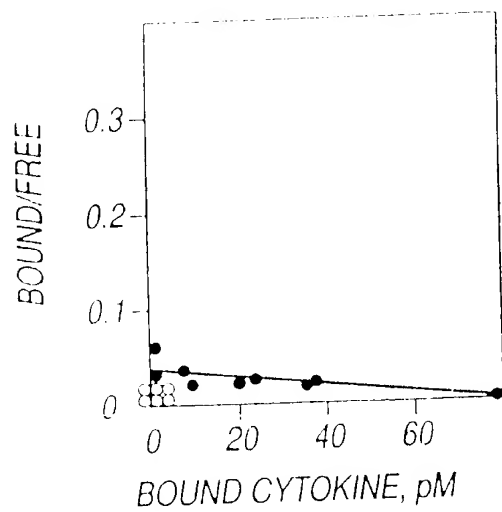


Fig. 3(A)

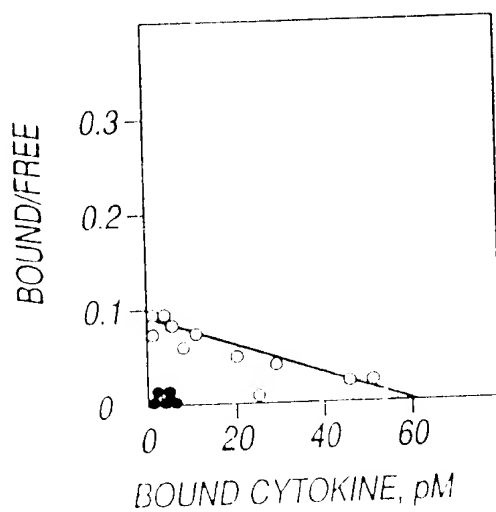


Fig. 3(B)

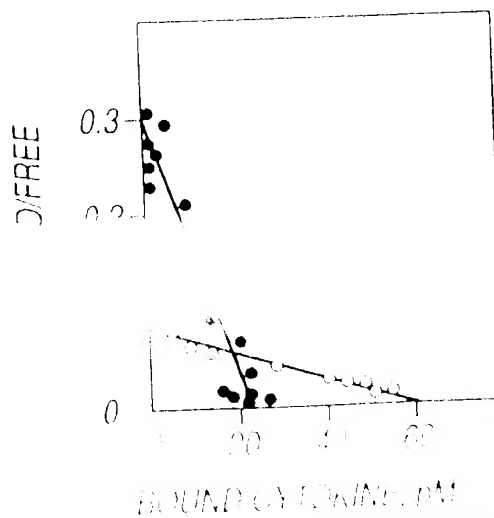
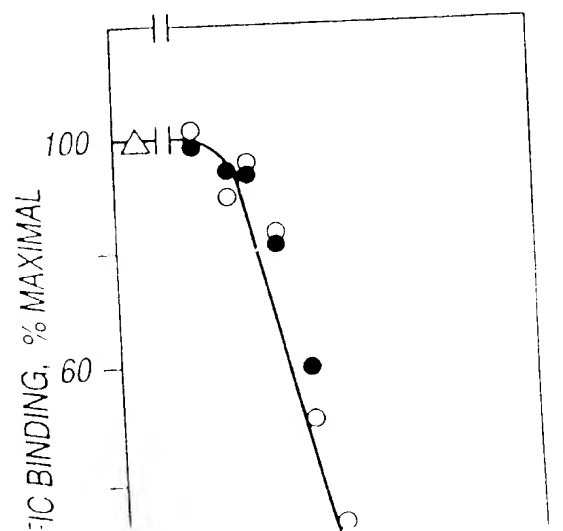
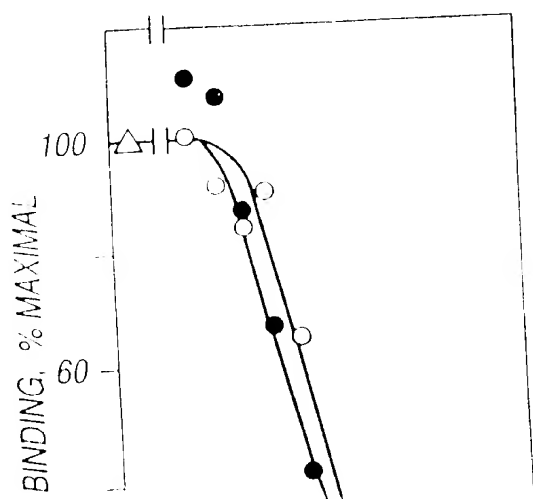
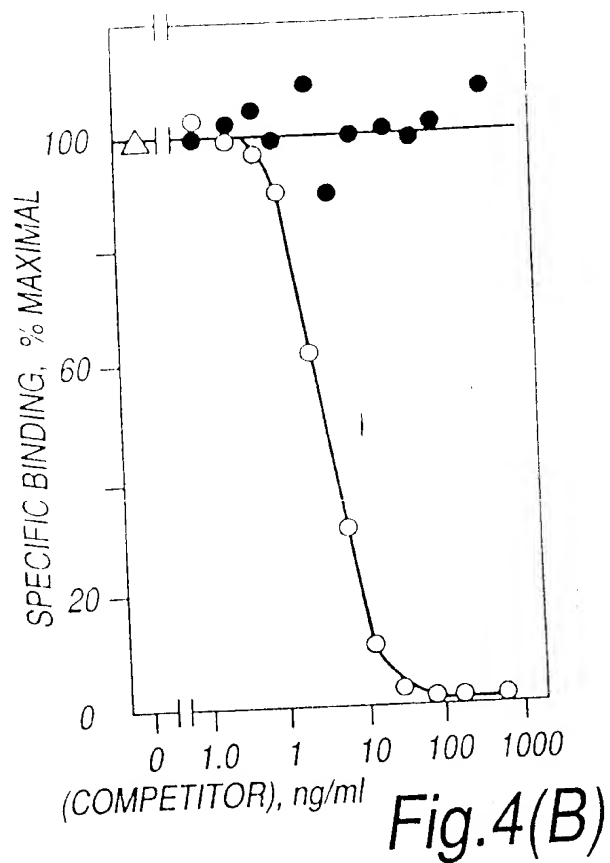
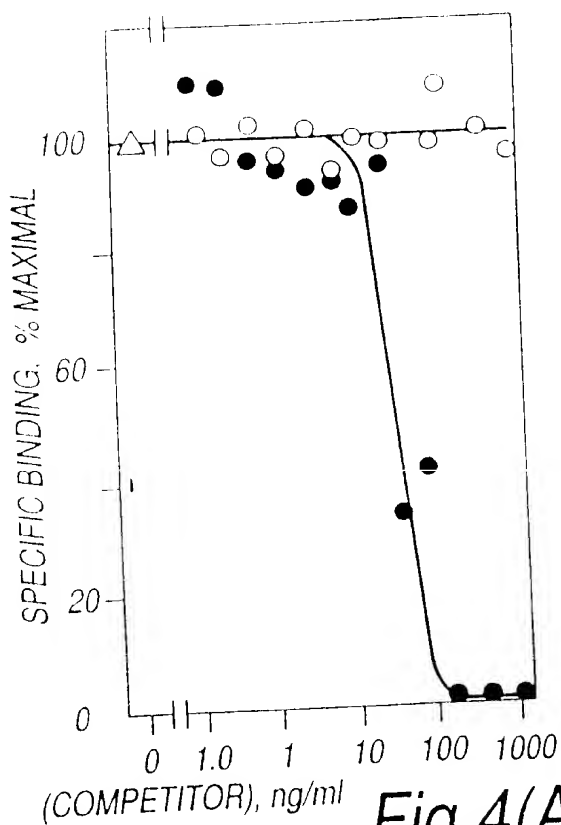


Fig. 3(C)

10/24



11/24

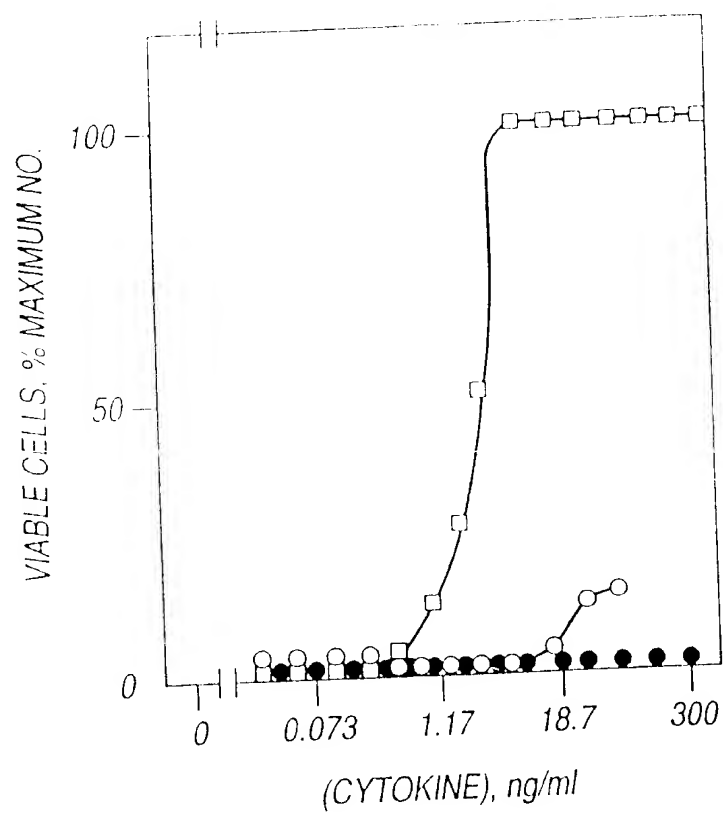
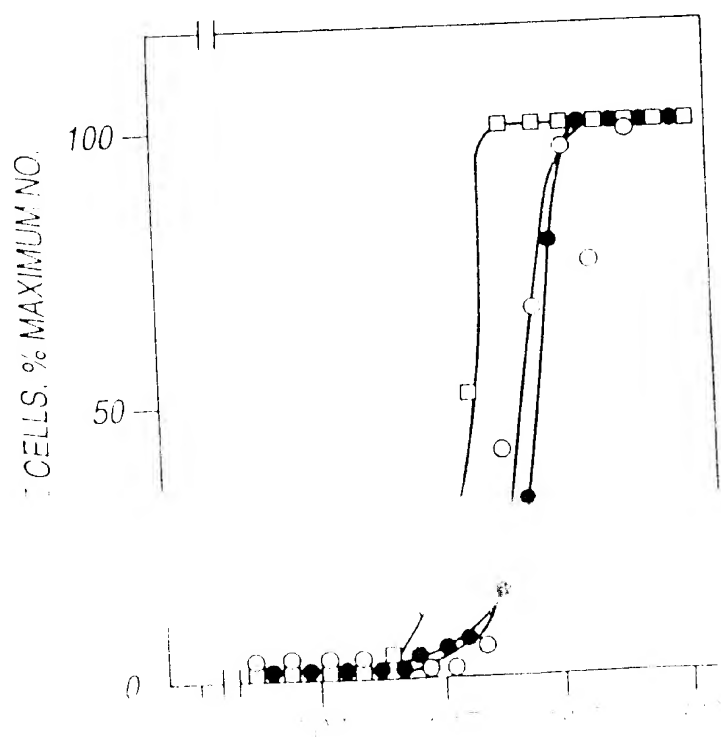


Fig. 5(A)



12/24

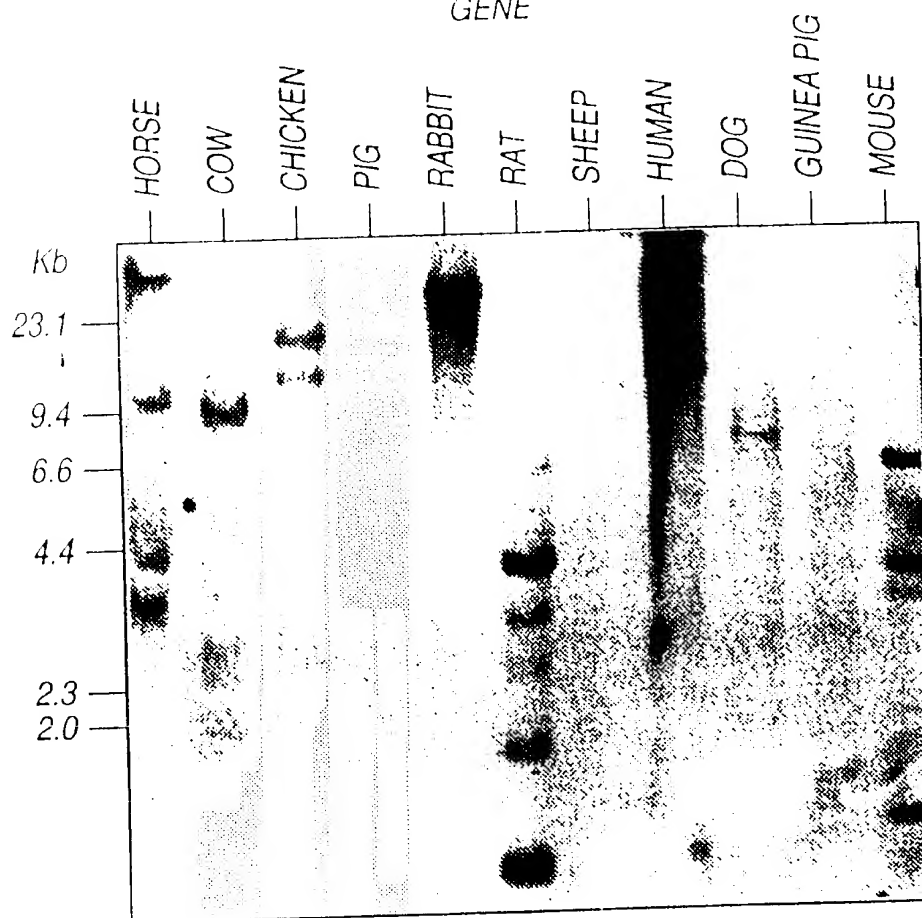
CROSS-SPECIES CONSERVATION OF THE NR-4 (IL-13R α)
GENE

Fig. 6

(major)

DYKDD DDYKD DDESR TEVQP PVTXL SV
 1 5 10 15 20 25

ASISS SDYKD DDESR TEVQP PVTXL SV
 1 5 10 15 20 25

13/24

14/24	15/24
16/24	17/24
18/24	19/24
20/24	21/24
22/24	23/24

Fig. 7

15/24

acgtgcgggccgggttccgagggcgagaggetgc

.....
cgaattcgggcacgagccgagggcgagggcctgc

L W A L L L C A G G G G
TGTGGGCGCTGCTGCTCTGCGCCGGCGGCGGGGGC

* * * *

TCTTGGTGCTGCTACTCTGGACCGCCACCGTG - -

L L V L L L W T A T V -

Q P P V T N L S V S V
AGCCACCTGTGACAAATTTGAGTGTCTCTGTT

* * * * *

AGCCACCTGTGACGAATTTGAGCGTCTCTGTC

Q P P V T N L S V S V

W N P P E G A S S N C
GGAATCCACCCGAGGGAGCCAGCTCAAATTGT

* * * * *

GGAGTCCTCCTGAAGGAGCCAGTCCAAATTGC

W S P P E G A S P N C

D K Q D K K I A P E T
ACAAACAAGATAAGAAAATAGCTCCGGAAACT

* * * * *

ACCAACAGGATAAGAAAATTGCTCCAGAAACT

Fig. 7(ii)

16/24

H		R R S I E V P L N
H		CGTCGTTCAATAGAAGTACCCCTGAATG
		* * * *
M	241	CATCGTAAAGACGAATTACCCCTGGATG
M	81	H R K E E L P L D
H		S T N E S E K P S
H		AGCACCAATGAGAGTGAGAAGCCTAGCA
		* * * * *
M	301	AGTGCCAATGAAAGTGAGAAGCCTAGCC
M	101	S A N E S E K P S
H		G D P E S A V T E
H		GGTGATCCTGAGTCTGCTGTGACTGAAC
		* * * * *
M	361	GGTGATCCTGAGTCCGCTGTGACTGAGC
M	121	G D P E S A V T E
H		K C S W L P G R N
H		AAGTGTTCTTGGCTCCCTGGAAGGAATA
		* * * * *
M	421	AAGTGTTCTTGGCTCCCTGGAAGGAATA
M	141	K C S W L P G R N
H		W H R S L E K I H
		TCCGACAGAGCCTGGAAAAATTCATC

Fig. 7(iii)

17/24

E R I C L Q V G S Q C
 AGAGGATTTGTCTGCAAGTGGGGTCCCAGTGT

* * * * *

AGAAAATCTGTCTGCAGGTGGGCTCTCAGTGT
 E K I C L Q V G S Q C

I' L V E K C I S P P E
 TTTTGGTTGAAAAATGCATCTCACCCCCAGAA

* * * * *

CTTTGGTGAAAAAGTGCATCTCACCCCCTGAA
 P L V K K C I S P P E

L Q C I W H N L S Y M
 TTCAATGCATTTGGCACAACCTGAGCTACATG

* * * * *

TCAAGTGCATTTGGCATAACCTGAGCTATATG
 L K C I W H N L S Y M

T S P D T N Y T L Y Y
 CCAGTCCCCGACACTAACTATACTCTCTACTAT

* * * * *

CAAGCCCTGACACACACTATACTCTGTACTAT
 T S P D T H Y T L Y Y

L O C E N I F R E G Q Y

Fig. 7(iv)

18/24

```

      *      *      *      *      *
M  481  TGGTACAGCAGCCTGGAGAAAAGTCGTC
M  161   W  Y  S  S  L  E  K  S  R

      F  G  C  S  F  D  L  T  K
H      TTTGGTTGTTTCCTTTGATCTGACCAAAG
H
      *      *      *      *      *      *
M  541  ATTGCTTGTTTCCTTTAAATTGACTAAAG
M  181   I  A  C  S  F  K  L  T  K

      Q  I  M  V  K  D  N  A  G
H      CAAATAATGGTCAAGGATAATGCAGGAA
H
      *      *      *      *      *      *      *      *
M  601  CAAATAATGGTCAAGGATAATGCTGGGA
M  201   Q  I  M  V  K  D  N  A  G

      T  S  R  V  K  P  D  P  P
H      ACTTCCCGTGTGAAACCTGATCCTCCAC
H
      *      *      *      *      *      *      *
M  661  ACTTCCTATGTGAAACCTGATCCTCCAC
M  221   T  S  Y  V  K  P  D  P  P

      L  Y  V  Q  W  E  N  P  Q
H      CTATATGTGCAATGGGAGAATCCACAGA
H
      *      *      *      *      *      *      *
M  721  TTATTAGTGCAGTGGAAGAATCCACAAA
M  741   T  I  V  Q  W  K  N  P  Q

```

Fig. 7(v)

19/24

* * * * *
AATGTGAAAACATCTATAGAGAAGGTCAACAC
Q C E N I Y R E G Q H
V K D S S F E Q H S V
TGAAGGATTCCAGTTTTGAACAACACAGTGTC
* * * * *
TCGAACCT - - AGTTTTGAACATCAGAACG TT
V E P - S F E H Q N V
K I K P S F N I V P L
AAATTAAACCATCCTTCAATATAGTGCCTTTA
* * * * *
AAATTAGGCCATCCTGCAAAATAGTGTCTTTA
K I R P S C K I V S L
H I K N L S F H N D D
ATATTAAAAACCTCTCCTTCCACAATGATGAC
* * * * *
ATATTAAACATCTTCTCCTCAAAAATGGTGCC
H I K H L L L K N G A
N F I S R C L F Y E V
ATTTTATTAGCAGATGCCTATTTTATGAAGTA
* * * * *
ATTTTAGAAGCAGATGCTTA ACTTATGAAGTG
* * * * *

Fig. 7(vi)

20/24

H		E	V	N	N	S	Q	T	E	T
H		GAAGTCAATAACAGCCAAACTGAGACAC								
		*	*	*	*		*	*		
M	781	GAGGTCAATAATACTCAAACCGACCGAC								
M	261	E	V	N	N	T	Q	T	D	R
H		E	N	P	E	F	E	R	N	V
H		GAGAATCCAGAATTTGAGAGAAATGTGG								
		*		*			*	*		
M	841	CAGAATTCCGAATCTGATAGAAACATGG								
M	281	Q	N	S	E	S	D	R	N	M
H		L	P	D	T	L	N	T	V	R
H		CTTCCTGATACTTTGAACACAGTCAGAA								
		*		*			*	*	*	
M	901	CTTGCCGACGCTGTCTACACAGTCAGAG								
M	301	L	A	D	A	V	Y	T	V	R
H		D	D	K	L	W	S	N	W	S
H		GATGACAAACTCTGGAGTAATTGGAGCC								
		*		*	*	*	*		*	*
M	961	GACAACAAACTGTGGAGTGATTGGAGTG								
M	321	D	N	K	L	W	S	D	W	S
H		T	L	Y	I	T	M	L	L	I

Fig. 7(vii)

21/24

```

H N V F Y V Q E A K C
ATAATGTTTTCTACGTCCAAGAGGCTAAATGT
* * * * *
ATAATATTTTAGAGGTTGAAGAGGACAAATGC
H N I L E V E E D K C
|
E N T S C F M V P G V
AGAATACATCTTGTTTCATGGTCCCTGGTGTT
* * * * *
AGGGTACAAGTTGTTTCCAACCTCCCTGGTGTT
E G T S C F Q L P G V

I R V K T N K L C Y E
TAAGAGTCAAAACAAATAAGTTATGCTATGAG
* * * * *
TAAGAGTCAAAACAAACAAGTTATGCTTTGAT
V R V K T N K L C F D

Q E M S I G K K R N S
AAGAAATGAGTATAGGTAAGAAGCGCAATTCC
* * * * *
AAGCACAGAGTATAGGTAAGGAGCAAAACTCC
E A Q S I G K E Q N S

V P V I V A G A I I V
|

```

Fig. 7(viii)

22/24

```

      *      *      *      *      *      *
M  1021 ACCTTCTACACCACCATGTTACTCACCA
M  341   T  F  Y  T  T  M  L  L  T

      L  L  L  Y  L  K  R  L  K
H
H      CTCCTGCTTTACCTAAAAAGGCTCAAGA
      *      *      *      *      *      *
M  1081 CTCCTT TTTTACCTGAAAAGGCTTAAGA
M  361   L  L  F  Y  L  K  R  L  K

      K  I  F  K  E  M  F  G  D
H
H      AAGATTTTTTAAAGAAATGTTTGGAGACC
      *      *      *      *      *      *
M  1141 AAGATTTTTTAAAGAAATGTTTGGAGACC
M  381   K  I  F  K  E  M  F  G  D

      D  I  Y  E  K  Q  T  K  E
H
H      GACATCTATGAGAAGCAAACCAAGGAGG
      *      *      *      *      *      *
M  1201 GACATCTATGAGAAACAATCCAAAGAAG
M  401   D  I  Y  E  K  Q  S  K  E

      K  K  A  S  Q  *
H
H      AAGAAAGCCTCTCAGTGAtggagataat
      *      *      *
M  1261 AAGAAAGCAGCTCCTTGAtgggggagaag
M  421   K  K  A  A  P  *

```

Fig. 7(ix)

23/24

```

      *   *       *   *       *       *
TTCCAGTCTTTGTCTGCAGTGGCAGTCATAATC
I   P   V   F   V   A   V   A   V   I   I

I   I   I   F   P   P   I   P   D   P   G
TTATTATATTCCCTCCAATTCCTGATCCTGGC
*   *   *   *   *   *   *   *   *   *
TCATTATATTTCCCTCCAATTCCTGATCCTGGC
I   I   I   F   P   P   I   P   D   P   G

Q   N   D   D   T   L   H   W   K   K   Y
AGAATGATGATACTCTGCACTGGAAGAAGTAC
*   *   *   *   *   *   *   *   *   *
AGAATGATGATACCCTGCACTGGAAGAAGTAT
Q   N   D   D   T   L   H   W   K   K   Y

E   T   D   S   V   V   L   I   E   N   L
AAACCGACTCTGTAGTGCTGATAGAAAACCTG
*   *   *   *   *   *   *   *   *   *
AAACGGATTCTGTAGTGCTGATAGAAAACCTG
E   T   D   S   V   V   L   I   E   N   L

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tgattttctttcttgccttcaatgtgaccctgt

```

Fig. 7(x)

24/24

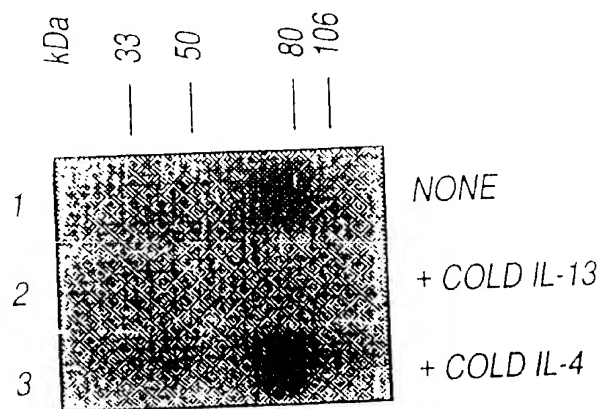


Fig. 8

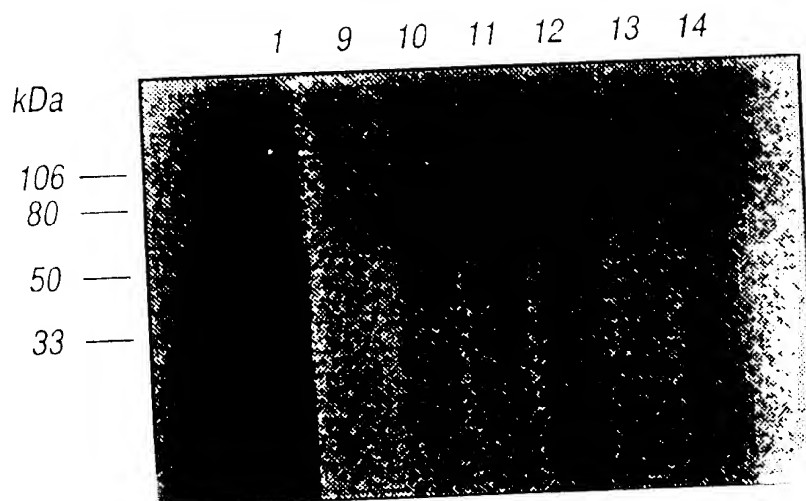


Fig. 9